

Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



FIG. 1B

Patched motif

Patched

Consensus 1 VLSSKIRYTPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPIISRSFIIITAKARNS-NILDIR/LNEVVQVNDFTSTNV 78
HTPL-L 162 deeedleehYTPVGSAPAKAERRFVQGHFTTndSYRFSASRRSTEANFVSLVVSYS- SLDDPA'FAEVSKLDGAVQDLR 240
gi 1825729 47 NPLSDAVLFTPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTSQREIQVTALARNDSNILDPKFANAVYQLDKYIQTRV 125
gi 1707052 22 NVVYSLLMIFGPY---SYTERRIIHDAWPL-VDGTFVAGRAVTSQREVQAVVARSGGNILDRVFSNELKLMESEFIRNNI 97
gi 3892144 49 LRVDDPYSYVFTPSDARWRREISVFENENWPL-DENKFLPGKSFKAIRFVNILIRAKDGGSIMRDNV/LHEIEILNQWIMNNI 127

Consensus 79 TIPVSG--ITLSFKDLCMRFCDCINCPVNHQYNGQILRSN/HNSRIDLTYP'TMTFFGTKIYLGPNFGVKLDPN---PGN- 152
HTPL-L 241 VAREKG--SQIQYQVCARYALCVPPNPILYAWQVKNLTNLS--SISFPAYNHGRHPLVLTGFFGVILGGS---LGMg 313
gi 1825729 126 RVLHNG--HYYSYKNLCLQYKNGGCPSPKHV---HILSDLNHGHNITYPYFRFGSEGGYIGSSIGGVTVMKgeneTDI- 199
gi 1707052 98 TVQFSN--RTWSFADLCCLAGpDGRCANNDHI---QLASRLHQHGHNITYPTVRLSDKSAIYASAIAGGVKLAKgdngeNI- 171
gi 3892144 128 SIPTDDI1kFNLTQDLCLSY-DWVCGANEHIQ-MLLRRNDVNQILDHLHFRPGGTKDTPVVLGGIFGVDVQFFQn----GT- 200



FIG. 1B

Patched motif (Continued)

	170	180	190	200	210	220	230	240	
consensus	153	154	155	156	157	158	159	160	
HTPL-L	161	162	163	164	165	166	167	168	
gi 1825729	169	170	171	172	173	174	175	176	
gi 1707052	177	178	179	180	181	182	183	184	
gi 3892144	185	186	187	188	189	190	191	192	
	250	260	270	280	290	300	310	320	
consensus	227	228	229	230	231	232	233	234	
HTPL-L	235	236	237	238	239	240	241	242	
gi 1825729	243	244	245	246	247	248	249	250	
gi 1707052	251	252	253	254	255	256	257	258	
gi 3892144	259	260	261	262	263	264	265	266	
	330	340	350	360	370	380	390	400	
consensus	294	295	296	297	298	299	300	301	
HTPL-L	302	303	304	305	306	307	308	309	
gi 1825729	310	311	312	313	314	315	316	317	
gi 1707052	318	319	320	321	322	323	324	325	
gi 3892144	326	327	328	329	330	331	332	333	
	410	420	430	440	450	460	470	480	
consensus	371	372	373	374	375	376	377	378	
HTPL-L	379	380	381	382	383	384	385	386	
gi 1825729	387	388	389	390	391	392	393	394	
gi 1707052	395	396	397	398	399	400	401	402	
gi 3892144	403	404	405	406	407	408	409	410	

FIG. 1



FIG. 1B

Patched motif (Continued)

	490	500	510	520	530	540	550	560
consensus*.....*.....*.....*.....*.....*.....*.....							
HTPL-L	-----SSKSHE--AEQ--AVVKFFLNICYPFLLNPKVRVCVLLVVLVLAIAIYCTNMKEGLDPAKL	475						
gi 1825729	-----SVPDEHgcdih--PMSLFFRDYFGPFLTRSESKYFVFIYVLYIISIIYGFHVGQEGDLRNL	632						
gi 1707052	-----HSASHD--VKQp-LTSRFFGEWYAPVLMHPVVRGIAMVWFVIYLLGASVGCSSRIKEGLEPVL	528						
gi 3892144	-----tssvstmtsqatSPASKH--LHHC-AATSFRRWYAPVLMQPIRAIAGLWVLIYLGISVIGCTHLKEGLEPVL	522						
gi 3892144	-----ipaeafawkeqgspnsISKKSKD--REEkdRIVHFIGKIYGPPIFSLNSVRIFSGLIFVVLVLAIAIYGCYNFREGNPGNL	592						
consensus*.....*.....*.....*.....*.....*.....*.....*.....							
HTPL-L	-----FLKDSPLVEYLRLREKHVWPYGLQVTVFVNPPDLTNPENRDLNEMVDEFENTPYAMGNSTKFWLRDYENFLYSPISE	555						
gi 1825729	-----ASDSDSYITPYFNVEENYFSDYGPVVMIVTKKVDYWDKDVQRKLENTKIFEKVUY--VDKNLTFEFLDAYVQYLYK--GNS	709						
gi 1707052	-----LVEDSYAI PHYRLLeKYFWKYGQOQVIVINAPDLRNHTSRDRVHAMVLDFAATSKHAIGMESVQFVLFEMER--YYQKELE	607						
gi 3892144	-----VTNDHYIAKYFSDI-KHFWRIGAQHLHVAVLNPPNLTISENRNELLKVVSAPENTQYTLGREGTVFFLLEVLNLYLSELNAE	671						
consensus*.....*.....*.....*.....*.....*.....*.....*.....							
HTPL-L	-----LEDEEEWFYDLEWFL-KSPGFSHWVGDLVWDN-KTDYETTVIKKFRFTTGGKDLSTWTDTRLKLTWRGVADEYDFDN	633						
gi 1825729	-----QPNKNTFMNNIPDFLSNFPNFQH-----DI-NISSNEIISRGF-IQTTDVSSSAKKILLFQLRRIA-EDQIP	779						
gi 1707052	-----VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGpPDDNDGTMVKSFRFILGMDLVTTMDQTDATMSPREVAARWPEFN	685						
gi 3892144	-----IQYDN-EKFYDHAQYI-YSDMSQpWVDVWVG--RNNNSERI IKTRFRMIGMRDISTTTKQTEATNTFREIASRFEQYN	676						
gi 3892144	-----VEDTERLWTKLNSWLK-YTGGSTQWASNLKIN-----KTDGSFQAFRFQIALKNFVEPNHKAQAQLLRDIADHQP-FN	744						
consensus*.....*.....*.....*.....*.....*.....*.....*.....							
HTPL-L	-----VTVFDED-----AFFLDQILSIGPTTQSIITWTLICMAVVCFLFIPNPNTVFVITVSI	686						
gi 1825729	-----FMYDQYAAILEDVTRNVNLVSAAMFIVLSLLIPYPLCSLWTFAI	832						
gi 1707052	-----WMFTDQYIIIPNTVQIIIIALLVMIVIAVLFIQPMCSLWVALAC	738						
gi 3892144	-----WLFETDQYALVVNTMQDIIIVAVACMLVISALLIPQVCSFWAVTI	729						
gi 3892144	-----VVYHEVsfgnrkilndfissshcyaqknipklaFPFADQYLIILPATIQNVVVISLCAVVSFLNVPSPSGFVIFVSI	824						



FIG. 1B

Patched motif (Continued)

consensus	687	ASIDIGVFGFLSLWGVLDLPISMTIIMSIGFSVDFSAHIAHYFYSRSHGSETPDERLADALEALGWPIVQAALSTILCVL	766
HTPL-L	833	GSVIVGVTCGFMAFWKVNLDLSIMINLVICTGFSDFSAHISYAFV-SSSQPSVYNQKSVEALYLLGYFVLQSAISTIIIGVC	911
gi 1825729	739	ASIDFGVIGYMTLWGVNLDIAISMTIIMSIGFSVDYSAHIAHYGVVVSRED-TAAGRVKESALCWPLSQGAMSTIIAIVS	817
gi 1707052	730	GSIDLGVIGFMTLWVNLDIAISMTIIMSIGFSVDYSAHITYAVVISKES-TTSARVCDALGDLCWVPAQGMSTILAVS	808
gi 3892144	825	VSINIGVFGYMTLWGVNLDVAVSMISLIIMSIGFAVDLSAHIYAFVTSHG--DTKQRVIGALETLGWPIFQGSASSTIAGIS	902
consensus	767	PLLFVPSYMWVVFVKTFIFLVVVGILLHGLIFLPILSLFVT-----IRTSNAKIKKPSSI	821
HTPL-L	912	VLAARAYIFRTFFKIMFLVMIFGAHGLIFIPVFLTFGRfi-----	954
gi 1825729	818	VLADIPAYMIVTFFKTVVLSISLGLLHGLVFLPVLLSIFVRGCCIPSPSPHCHPSAQKIEKQIRI	882
gi 1707052	809	VLSDVPAYMIVTFFKTVFLAISIGFLHGLVFLPLMLSVFVGki-----fdIHISNISIKYCIYL	867
gi 3892144	903	ILYTVDAVILVFFKTIWLTMLIGAIHGLFFIPIFLSLFPV-----EFFRIPKSSEL	954



Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



FIG. 1B

Patched motif

Patched

Consensus	1	VLSSKIRYTF	10	20	30	40	50	60	70	80	
HTPL-L	162	deeedleehYTPV	20	30	40	50	60	70	80		
gi 1825729	47	NPLSDAVLFTPL	10	20	30	40	50	60	70	80	
gi 1707052	22	NVYSLLMIFGPY	10	20	30	40	50	60	70	80	
gi 3892144	49	LRVDDPSYVFT	10	20	30	40	50	60	70	80	
Consensus	79	TIPVSG--ITL	90	100	110	120	130	140	150	160	
HTPL-L	241	VAREKG--SQI	90	100	110	120	130	140	150	160	
gi 1825729	126	RVLHNG--HY	90	100	110	120	130	140	150	160	
gi 1707052	98	TVQFSN--RT	90	100	110	120	130	140	150	160	
gi 3892144	128	SIPTDDlkFN	90	100	110	120	130	140	150	160	



FIG. 1B

Patched motif (Continued)

```

170 180 190 200 210 220 230 240
.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 153 --IKSVKAIIVLYRLKRDPEEEDSKEWELSLFDYLENEYASD-HIQ-VTIFSDQVLED--ELVRNGLTLPFFVVGFA 226
HTPL-L 314 qLLLRKAMRLLYLKTEDEYDVQSQWLTHLDQFTNIKIL-ALKKIEVHFYSLSRqLBEFATSVTVIPVFHLAYI 392
gi 1825729 200 --LASAKAWFMIYHLKFHPEMSYISGEWELELGRMLTQYEDP-YIS-ITYFHSQTLAD--ELKRNADTLIPRFIIISIT 273
gi 1707052 172 --IVEATAWLLIYQLKFYPNEISYVSGLWEREFKNMDEYKKQAKYIS-ITYFHSQTLSD--ELNRNAERLAPKFIGAFV 246
gi 3892144 201 --LSDAKLTQLFYFLKQDQKMVEEYSSKFSYALETFLNQVYSSD-VIT-LSFAHYQSLED--GLDENAKAFVFNFVVSFF 274

250 260 270 280 290 300 310 320
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 227 ILVFTSILTSVRLAS-GSLHIDWRSKPILAILGLVLTPLMAIVSAFGLLFWLGFRENSIVCMPPFLVL----- 293
HTPL-L 393 LIILFAVTSCRF-----DCIRNKMVAAFGVISAFVAVSGFGLLHIGVPFVIIVANSPFLIL----- 452
gi 1825729 274 LLIVFSTLCSLSFID-GSFSIDWLSKPILSILGVWSAGIAITLTVGVFLSLGMPYNDIVGVMPFLVL----- 340
gi 1707052 247 ILVCFSVLCISVITIK-GSGVIDWVTKPILSVLGVSNAGMGIASAMGLTYLEIQYNDIIAVNPPFLV----- 313
gi 3892144 275 VLAMVALVSSFTLKSSSATKIDWISSKPWLAAGMFSTVLSIISAFGLFLILGVRYNVINTIIPFLIIgefgsfkmeKn 354

330 340 350 360 370 380 390 400
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 294 ---AIGVDDMFLMVHAWQRTTRSLSVKKRMGEVLEEAGPSITITSLTNVLSFGIGAITPTPEIQLFQCIYTAVAIFDFIY 370
HTPL-L 453 ---GVGVDDMFIMISAWHKTNLGDIRMSNVYSKAAVSITITITNLALYTGIMSSFRSQCFIYTGITLLFCYFY 529
gi 1825729 341 ---AVGVDDNFMVAAVRRTSRTHVHERMGECIADAAVSILITSSDVLDFGVGAITTPAVQIFCVYTGVAIFFAFIY 417
gi 1707052 314 ---AVGTDNFMFLVASLKRTRNLKVDQRIAECDADAAVSILITALTALDFGVGTITTPAVQIFCIYTMCAILLTFAY 390
gi 3892144 355 qIPaIGIDDMMFLMNACWDQTSKLSVPERMSKTLSHAGVAVITNVTDMVSFAIGCITDLPQIGQFFCIYACVSAFSYFY 434

410 420 430 440 450 460 470 480
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 371 QLTPFAAIMAIAAGKYEMKGRHSLFLR---AVDAAETESP---QRLDSRGSAGAK----- 416
HTPL-L 530 NITFCGAFMALDCKRE---VVCCLW---LKADPKWPS---FKFCCFPFG----- 571
gi 1825729 418 QITFAACIALAMKHEASGRNSLFLIE---AVSAEKKTSLSLst--fQRLFNLGSVpQd----- 468
gi 1707052 391 QLTPFCAILVYVTRIEEQGLHSLWLRp---AVTVSSSTSLN---VKLFWLGSQpKpplpsctvss----- 450
gi 3892144 435 QLTPFSGAIAINGEVEREKRHCLFFYrtfqLVDISKMNEEadsklQIKRSASpafpnylssnsfssdsdsfsskkt 514
```




FIG. 1B

Patch d motif (Continued)

consensus	687	ASIDIGVFGFLSLWGVLDLPISMITIIMSIGFSDFS	810	820	830	840	850	860	870	880
HTPL-L	833	GSVIVGVTGEMAFWKVNLD	810	820	830	840	850	860	870	880
gi 1825729	739	ASIDFGVIGYMTLWGVNLD	810	820	830	840	850	860	870	880
gi 1707052	730	GSIDLGVLGFTLWVNLD	810	820	830	840	850	860	870	880
gi 3892144	825	VSINIGVFGYMTLWGVNLD	810	820	830	840	850	860	870	880
consensus	767	PLLFVPSYMWVFFKTI	890	900	910	920	930	940		
HTPL-L	912	VLAARAYIFRTFFKIMFLVMIFGAHGLIFIPVLT	890	900	910	920	930	940		
gi 1825729	818	VLADIPAYMIVTFFKTVLSISLGLHGLVFLPVL	890	900	910	920	930	940		
gi 1707052	809	VLSVPAYMIVTFFKTVFLAISIGFLHGLVFLPVL	890	900	910	920	930	940		
gi 3892144	903	ILYTVDAYIILVFFKTIWLTMLIGAIHGLFFIPI	890	900	910	920	930	940		